



wwPDB X-ray Structure Validation Summary Report

May 19, 2014 – 10:33 PM EDT

PDB ID : 1GPH
Title : STRUCTURE OF THE ALLOSTERIC REGULATORY ENZYME OF
PURINE BIOSYNTHESIS
Authors : Smith, J.L.
Deposited on : 1994-04-20
Resolution : 3.00 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

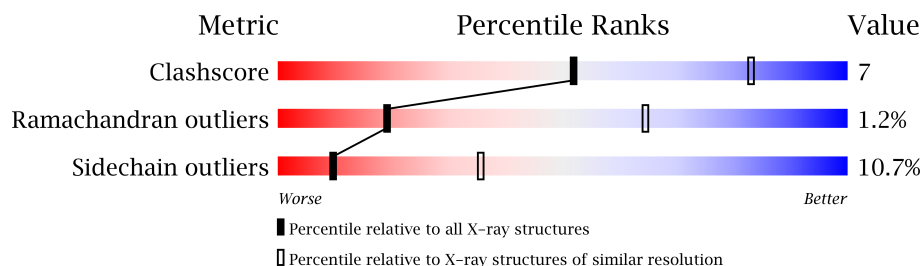
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22978

1 Overall quality at a glance

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1594 (3.00-3.00)
Ramachandran outliers	78287	1537 (3.00-3.00)
Sidechain outliers	78261	1540 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	1	465	
1	2	465	
1	3	465	
1	4	465	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14676 atoms, of which 304 are hydrogens and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

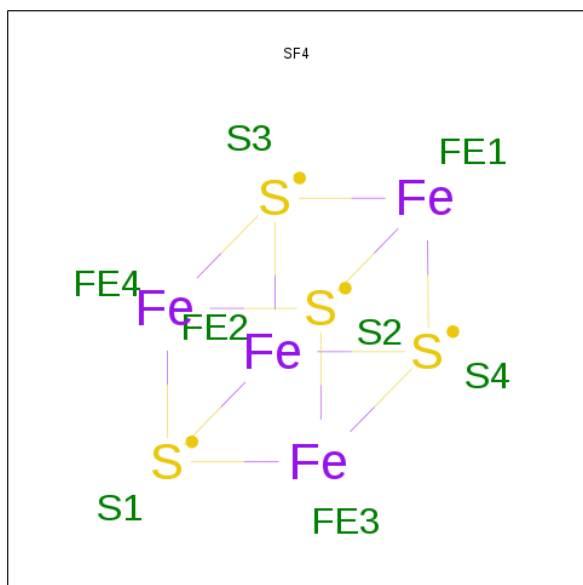
- Molecule 1 is a protein called GLUTAMINE PHOSPHORIBOSYL-PYROPHOSPHAT EAMIDOTRANSFERASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	1	465	Total	C	H	N	O	S	0	0	0
			3615	2212	76	620	687	20			
1	2	465	Total	C	H	N	O	S	0	0	0
			3615	2212	76	620	687	20			
1	3	465	Total	C	H	N	O	S	0	0	0
			3615	2212	76	620	687	20			
1	4	465	Total	C	H	N	O	S	0	0	0
			3615	2212	76	620	687	20			

There are 4 discrepancies between the modelled and reference sequences:

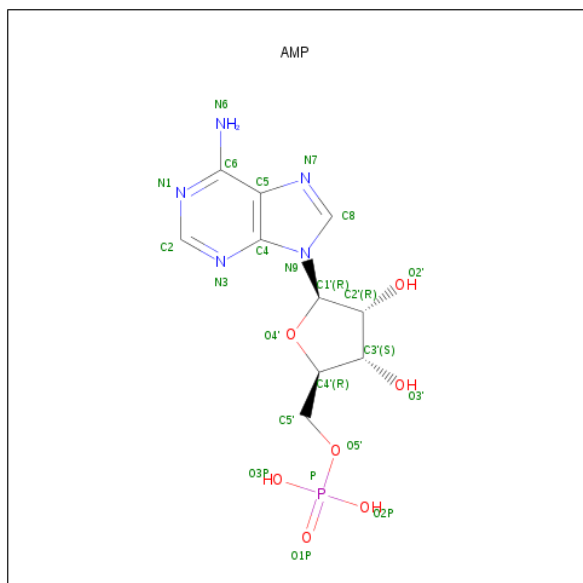
Chain	Residue	Modelled	Actual	Comment	Reference
1	402	ASP	GLY	CONFLICT	UNP P00497
2	402	ASP	GLY	CONFLICT	UNP P00497
3	402	ASP	GLY	CONFLICT	UNP P00497
4	402	ASP	GLY	CONFLICT	UNP P00497

- Molecule 2 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	1	1	Total	Fe	S	0	0
			8	4	4		
2	2	1	Total	Fe	S	0	0
			8	4	4		
2	3	1	Total	Fe	S	0	0
			8	4	4		
2	4	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 3 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	1	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	1	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	2	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	2	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	3	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	3	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	4	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	4	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

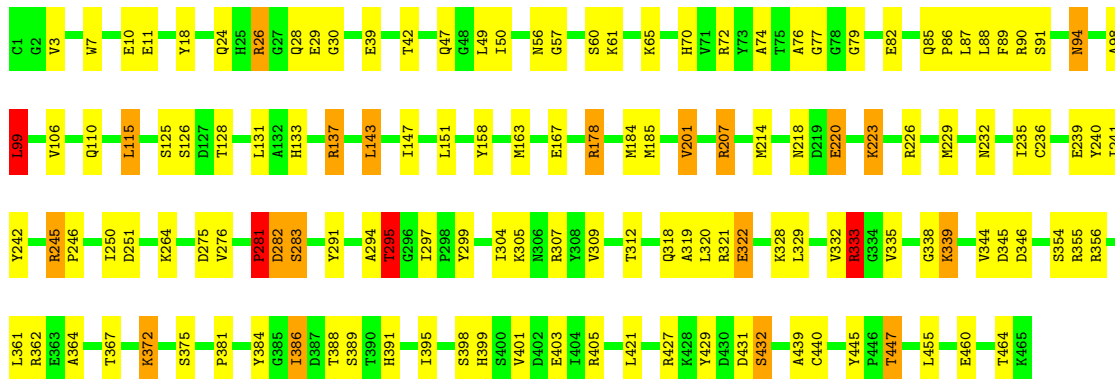
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

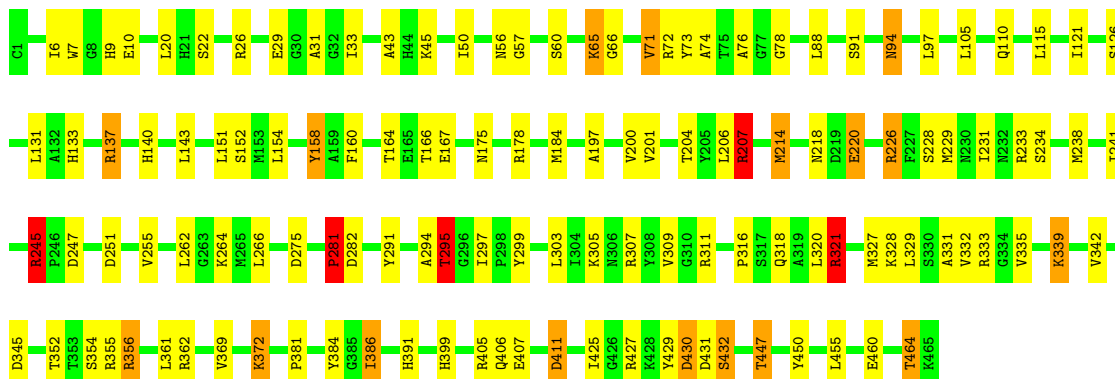
- Molecule 1: GLUTAMINE PHOSPHORIBOSYL-PYROPHOSPHATEAMIDOTRANSFERASE

Chain 1: 



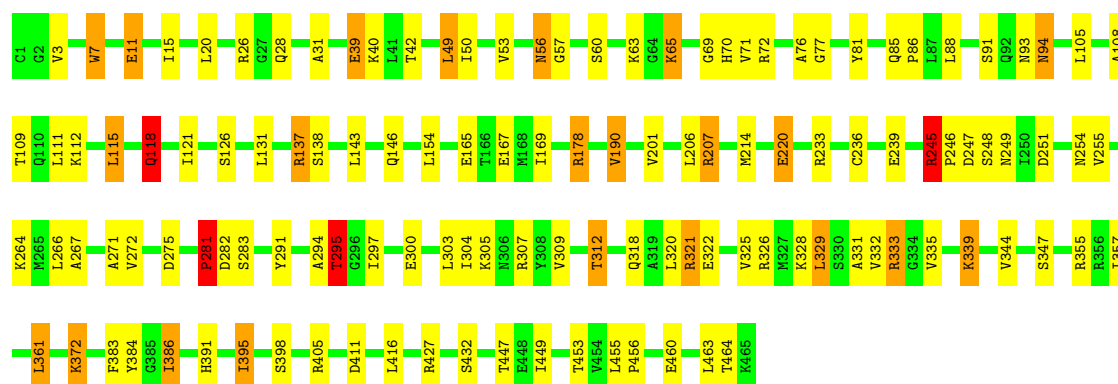
- Molecule 1: GLUTAMINE PHOSPHORIBOSYL-PYROPHOSPHATEAMIDOTRANSFERASE

Chain 2: 



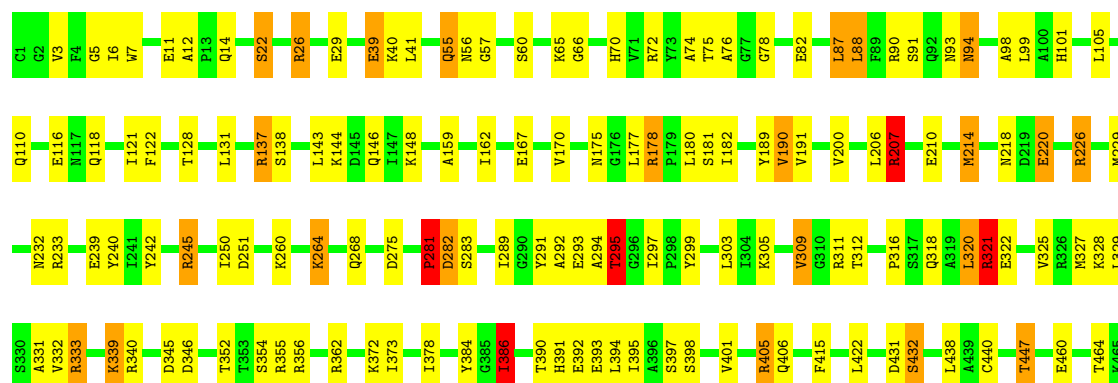
- Molecule 1: GLUTAMINE PHOSPHORIBOSYL-PYROPHOSPHATEAMIDOTRANSFERASE

Chain 3: 



• Molecule 1: GLUTAMINE PHOSPHORIBOSYL-PYROPHOSPHATEAMIDOTRANSFERASE

Chain 4:



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	158.80Å 75.70Å 94.10Å 90.00° 91.40° 90.00°	Depositor
Resolution (Å)	7.00 – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) (7.00-3.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.182 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	14676	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: AMP, SF4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.86	1/3597 (0.0%)	1.63	51/4857 (1.1%)
1	2	0.82	0/3597	1.58	47/4857 (1.0%)
1	3	0.84	1/3597 (0.0%)	1.59	42/4857 (0.9%)
1	4	0.82	0/3597	1.60	45/4857 (0.9%)
All	All	0.83	2/14388 (0.0%)	1.60	185/19428 (1.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	3	190	VAL	CA-CB	5.40	1.66	1.54
1	1	375	SER	CA-CB	-5.08	1.45	1.52

The worst 5 of 185 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	4	26	ARG	NE-CZ-NH1	14.54	127.57	120.30
1	1	281	PRO	CA-C-N	-12.07	90.65	117.20
1	3	207	ARG	NE-CZ-NH1	11.48	126.04	120.30
1	3	207	ARG	NE-CZ-NH2	-11.36	114.62	120.30
1	2	427	ARG	NE-CZ-NH1	11.36	125.98	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	18	TYR	Sidechain

5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	3539	76	3448	51	0
1	2	3539	76	3448	46	0
1	3	3539	76	3448	56	0
1	4	3539	76	3448	63	0
2	1	8	0	0	2	0
2	2	8	0	0	0	0
2	3	8	0	0	0	0
2	4	8	0	0	0	0
3	1	46	0	24	2	0
3	2	46	0	24	0	0
3	3	46	0	24	1	0
3	4	46	0	24	1	0
All	All	14372	304	13888	206	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

The worst 5 of 206 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:4:275:ASP:HB2	1:4:339:LYS:HG3	1.61	0.82
1:4:41:LEU:HD12	1:4:88:LEU:HD21	1.63	0.81
1:4:316:PRO:HG2	1:4:321:ARG:HD3	1.68	0.75
1:3:264:LYS:HG2	1:3:294:ALA:HB2	1.69	0.74
1:1:291:TYR:O	1:1:295:THR:HB	1.92	0.68

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	463/465 (100%)	436 (94%)	19 (4%)	8 (2%)	14	54
1	2	463/465 (100%)	433 (94%)	23 (5%)	7 (2%)	15	58
1	3	463/465 (100%)	437 (94%)	23 (5%)	3 (1%)	33	81
1	4	463/465 (100%)	434 (94%)	24 (5%)	5 (1%)	21	67
All	All	1852/1860 (100%)	1740 (94%)	89 (5%)	23 (1%)	19	64

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	56	ASN
1	2	282	ASP
1	2	431	ASP
1	3	94	ASN
1	4	56	ASN

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	382/382 (100%)	339 (89%)	43 (11%)	9	33
1	2	382/382 (100%)	343 (90%)	39 (10%)	11	38
1	3	382/382 (100%)	340 (89%)	42 (11%)	9	34
1	4	382/382 (100%)	343 (90%)	39 (10%)	11	38
All	All	1528/1528 (100%)	1365 (89%)	163 (11%)	10	35

5 of 163 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	2	372	LYS
1	3	109	THR
1	4	320	LEU
1	2	399	HIS
1	3	11	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	3	391	HIS
1	4	391	HIS
1	4	315	GLN
1	2	391	HIS
1	4	55	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SF4	1	466	1	12,12,12	8.08	12 (100%)	0,24,24	0.00	-
3	AMP	1	467	-	25,25,25	1.21	3 (12%)	38,38,38	1.80	8 (21%)
3	AMP	1	468	-	25,25,25	1.10	1 (4%)	38,38,38	1.24	5 (13%)
2	SF4	2	466	1	12,12,12	8.58	11 (91%)	0,24,24	0.00	-
3	AMP	2	467	-	25,25,25	1.28	4 (16%)	38,38,38	1.48	7 (18%)
3	AMP	2	468	-	25,25,25	1.55	4 (16%)	38,38,38	1.43	7 (18%)
2	SF4	3	466	1	12,12,12	8.64	12 (100%)	0,24,24	0.00	-
3	AMP	3	467	-	25,25,25	1.25	4 (16%)	38,38,38	1.38	6 (15%)
3	AMP	3	468	-	25,25,25	1.07	2 (8%)	38,38,38	1.49	4 (10%)
2	SF4	4	466	1	12,12,12	8.13	11 (91%)	0,24,24	0.00	-
3	AMP	4	467	-	25,25,25	0.93	1 (4%)	38,38,38	1.28	3 (7%)
3	AMP	4	468	-	25,25,25	1.12	2 (8%)	38,38,38	1.40	5 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SF4	1	466	1	-	0/0/48/48	0/6/5/5
3	AMP	1	467	-	-	0/10/26/26	0/3/3/3
3	AMP	1	468	-	-	0/10/26/26	0/3/3/3
2	SF4	2	466	1	-	0/0/48/48	0/6/5/5
3	AMP	2	467	-	-	0/10/26/26	0/3/3/3
3	AMP	2	468	-	-	0/10/26/26	0/3/3/3
2	SF4	3	466	1	-	0/0/48/48	0/6/5/5
3	AMP	3	467	-	-	0/10/26/26	0/3/3/3
3	AMP	3	468	-	-	0/10/26/26	0/3/3/3
2	SF4	4	466	1	-	0/0/48/48	0/6/5/5
3	AMP	4	467	-	-	0/10/26/26	0/3/3/3
3	AMP	4	468	-	-	0/10/26/26	0/3/3/3

The worst 5 of 67 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	4	466	SF4	S1-FE2	-12.95	2.24	2.33
2	3	466	SF4	S1-FE2	-12.71	2.24	2.33
2	1	466	SF4	S4-FE3	-12.53	2.24	2.33
2	4	466	SF4	S4-FE3	-12.32	2.25	2.33
2	2	466	SF4	S1-FE2	-12.22	2.25	2.33

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	1	467	AMP	C3'-C2'-C1'	5.66	109.80	100.92
3	4	468	AMP	C4'-O4'-C1'	-5.01	104.21	109.72
3	1	467	AMP	P-O5'-C5'	4.51	130.17	118.63
3	3	468	AMP	C8-N9-C4	-4.21	103.53	106.96
3	3	468	AMP	C3'-C2'-C1'	3.96	107.13	100.92

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.